

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/907,263

DATE: 08/13/2001

TIME: 13:28:55

Input Set : N:\Crf3\RULE60\09907263.txt
 Output Set: N:\CRF3\08132001\I907263.raw

72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

74 GAT	AGT	GTG	TGT	CCC	CAA	GGA	AAA	TAT	ATC	CAC	CCT	CAA	AAT	AAT	TCG		48
75 Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser		
76 1				5					10				15				
78 ATT	TGC	TGT	ACC	AAG	TGC	CAC	AAA	GGA	ACC	TAC	TTG	TAC	AAT	GAC	TGT		96
79 Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys		
80				20				25				30					
82 CCA	GGC	CCG	GGG	CAG	GAT	ACG	GAC	TGC	AGG	GAG	TGT	GAG	AGC	GGC	TCC		144
83 Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser		
84				35			40				45						
86 TTC	ACC	GCT	TCA	GAA	AAC	CAC	CTC	AGA	CAC	TGC	CTC	AGC	TGC	TCC	AAA		192
87 Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys		
88				50			55			60							
90 TGC	CGA	AAG	GAA	ATG	GGT	CAG	GTG	GAG	ATC	TCT	TCT	TGC	ACA	GTG	GAC		240
91 Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp		
92 65				70			75			80							
94 CGG	GAC	ACC	GTG	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	TGG		288
95 Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp		
96				85			90			95							
98 AGT	GAA	AAC	CTT	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG		336
99 Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly		
100			100			105			110								
102 ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC		384
103 Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys		
104			115			120			125								
106 CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	AGT	AAC		432
107 His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn		
108			130			135			140								
110 TGT	AAG	AAA	AGC	CTG	GAG	TGC	ACG	AAG	TTG	TGC	CTA	CCC	CAG	ATT	GAG		480
111 Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu		
112 145				150			155			160							
114 AAT															483		
115 Asn																	
119 (2) INFORMATION FOR SEQ ID NO: 2:																	
121 (i) SEQUENCE CHARACTERISTICS:																	
122 (A) LENGTH: 161 amino acids																	
123 (B) TYPE: amino acid																	
124 (D) TOPOLOGY: linear																	
126 (ii) MOLECULE TYPE: protein																	
128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:																	
130 Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser		
131 1				5			10			15							
133 Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys		
134				20			25			30							
136 Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser		
137				35			40			45							
139 Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys		
140				50			55			60							
142 Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp		

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143	65	70	75	80
145	Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp			
146	85	90	95	
148	Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly			
149	100	105	110	
151	Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys			
152	115	120	125	
154	His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn			
155	130	135	140	
157	Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu			
158	145	150	155	160
160	Asn			
163	(2) INFORMATION FOR SEQ ID NO: 3:			
165	(i) SEQUENCE CHARACTERISTICS:			
166	(A) LENGTH: 705 base pairs			
167	(B) TYPE: nucleic acid			
168	(C) STRANDEDNESS: unknown			
169	(D) TOPOLOGY: unknown			
171	(ii) MOLECULE TYPE: cDNA			
174	(ix) FEATURE:			
175	(A) NAME/KEY: CDS			
176	(B) LOCATION: 1..705			
179	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
181	TTG CCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC	48		
182	Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser			
183	1 5 10 15			
185	ACA TGC CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC	96		
186	Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys			
187	20 25 30			
189	AGC AAG TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC	144		
190	Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr			
191	35 40 45			
193	TCG GAC ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC	192		
194	Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu			
195	50 55 60			
197	TGG AAC TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT	240		
198	Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser			
199	65 70 75 80			
201	GAC CAG GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC	288		
202	Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys			
203	85 90 95			
205	ACC TGC AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC	336		
206	Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys			
207	100 105 110			
209	CGG CTG TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC	384		
210	Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala			
211	115 120 125			
213	AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG	432		
214	Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro			

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215	130	135	140	
217	GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG CCC CAC			480
218	Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His			
219	145	150	155	160
221	CAG ATC TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC AGG GAT GCA			528
222	Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala			
223	165	170	175	
225	GTC TGC ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA GGG GCA GTA			576
226	Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val			
227	180	185	190	
229	CAC TTA CCC CAG CCA GTG TCC ACA CGA TCC CAA CAC ACG CAG CCA ACT			624
230	His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr			
231	195	200	205	
233	CCA GAA CCC AGC ACT GCT CCA AGC ACC TCC TTC CTG CTC CCA ATG GGC			672
234	Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly			
235	210	215	220	
237	CCC AGC CCC CCA GCT GAA GGG AGC ACT GGC GAC			705
238	Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp			
239	225	230	235	
242	(2) INFORMATION FOR SEQ ID NO: 4:			
244	(i) SEQUENCE CHARACTERISTICS:			
245	(A) LENGTH: 235 amino acids			
246	(B) TYPE: amino acid			
247	(D) TOPOLOGY: linear			
249	(ii) MOLECULE TYPE: protein			
251	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:			
253	Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser			
254	1	5	10	15
256	Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys			
257	20	25	30	
259	Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr			
260	35	40	45	
262	Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu			
263	50	55	60	
265	Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser			
266	65	70	75	80
268	Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys			
269	85	90	95	
271	Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys			
272	100	105	110	
274	Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala			
275	115	120	125	
277	Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro			
278	130	135	140	
280	Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His			
281	145	150	155	160
283	Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala			
284	165	170	175	
286	Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val			

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287 180 185 190
289 His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
290 195 200 205
292 Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
293 210 215 220
295 Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
296 225 230 235

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09907263.txt

Output Set: N:\CRF3\08132001\I907263.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]